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GENE FLOW AND SIMULATION MODELING OF TRANSGENE SPREAD IN POPLAR

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Specific Aims - Risk assessment for transgenic trees presents special challenges because of the space and time scales involved, and because of the complex interplay of ecological, genetic, agronomic, and social factors. We are assessing potential risks of large-scale cultivation of fertile transgenic hybrid poplars (*Populus* spp.) in the Northwestern United States. To predict gene flow from transgenic plantations, it is necessary to understand both the dynamics of gene movement within and between populations, and the ability of hybrid trees to produce fit progeny. The main objectives of the research are to characterize gene flow, mating success, and long-distance pollen movement in wild poplar populations, measure gene flow from hybrid poplar plantations, study dispersal and establishment of seeds and vegetative propagules from hybrid plantations, compare establishment rates and relative competitiveness of hybrid and wild seedlings, create a spatial simulation model to project spread of poplar transgene across the landscape over time, and identify parameters most important in determining the extent of transgene spread.

Results - We have directly measured gene movement from non-transgenic hybrid plantations and in wild populations using molecular markers and paternity analysis methods. Average gene flow by pollen from plantations to wild populations ranged from 0.04% to 0.7% at three sites over two years. We are also studying gene flow among wild trees on a landscape scale at three sites. Gene flow was extensive in wild populations, with the majority of seeds being pollinated by trees more than 1 km away for most trees. This confirms that potential impacts of transgenic plantations must be considered over very large areas. We have also assessed establishment and competitiveness of hybrid seedlings in the wild. In 1996, hybrid seedlings established, survived and grew at higher rates than wild seedlings in artificially disturbed plots adjacent to plantations. However, hybrid and wild seedlings performed similarly in subsequent years and in common garden conditions. Furthermore, hybrid progeny comprised only about 1% of natural regeneration in the vicinity of plantations, and establishment of all seedlings was rare in space and time. Therefore, while there is substantial potential for gene flow from plantations, observed rates of

gene flow are relatively low. We are also conducting a mail and internet-based survey to assess potential consequences of herbicide resistance and insect resistance traits in wild and managed systems. We have targeted professionals with expertise in ecology, forestry, agriculture, vegetation control, and conservation. Thus far, forty-five people have responded to the survey, and we will conduct a further ten to twenty personal interviews. Using data from these gene flow studies, field trials, remote sensing databases, the survey, and the literature, we are developing a spatially explicit computer model to simulate transgene spread from plantations in the Pacific Northwest of the United States. Using digitized air photos and elevation maps, we have created a series of map layers depicting habitat types, land use, elevation, slope, aspect, and poplar population density, sex ratio, and age structure. These comprise the initial conditions for the model. The model will be used to identify the genetic and ecological parameters most critical to predicting the spread of herbicide and insect resistance transgenes over space and time. We will assess outcomes of the model and field studies in the context of the agronomic and ecological settings where the trees will be grown.

Plans for the Coming Year - In the coming year we will complete our analyses of gene flow from hybrid plantations and determine the importance of flowering time, tree size, and location for gene movement. We will complete coding the simulation model and perform 'virtual experiments' to determine the relative importance of factors such as fertility, fitness effects, and flooding for the spread of genes in the wild.

Publications:

DiFazio, S.P., S.Leonardi, S. Cheng, and S.H. Strauss. 1999. Assessing potential risks of transgene escape from fiber plantations. In P.W. Lutman (ed.) Gene flow and agriculture: relevance for transgenic crops. Symposium Proceedings No. 72. British Crop Protection Council, Farnham, UK. pp. 171-176.

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